

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Jeffrey E. Russell Examiner #: 62785 Date: 2-3-2005
 An Unit: 1654 Phone Number: 571-272-0969 Serial Number: 101705, 857
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL
REN 3C18(mailbox), 3D19(office)

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of invention: Effect on Calcium Channels To Prevent or Treat Wrinkles and Fine Lines

Inventors (please provide full names): B. Renault

Earliest Priority Filing Date: 11-13-2003

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO:2 (EEMQRR) in STN, in the US patent application sequence database (pending, published, + issued), and in Genoseq/Swisspat/PIR.

Thank you.

JER

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	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Junk _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep. Review Time _____	Fulltext _____	Sequence Systems _____
Clerical Prep. Time: _____	Patent Family _____	WWW/Internet _____
On line Time _____	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: February 5, 2005, 22:35:25 ; Search time 163 Seconds
(without alignments)
14.237 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	6	AA15582	AA15582 Human SNA
2	30	100.0	6	ADP13167	ADP13167 SNAP 25 p
3	30	100.0	13	AA15583	AA15583 Human SNA
4	30	100.0	13	ADP13168	ADP13168 SNAP 25 p
5	30	100.0	64	AAG00764	AAG00764 Human sec
6	30	100.0	82	AA15581	AA15581 Human SNA
7	30	100.0	82	ADP13166	ADP13166 SNAP 25 p
8	30	100.0	93	ABU43453	ABU43453 Protein e
9	30	100.0	106	AA15582	AA15582 Human sec
10	30	100.0	106	AA15582	AA15582 Human sec
11	30	100.0	198	AAU00255	AAU00255 Synapto
12	30	100.0	199	AAU00263	AAU00263 Synapto
13	30	100.0	200	AAU00264	AAU00264 Synapto
14	30	100.0	200	ADN11044	ADN11044 Murine SN
15	30	100.0	201	AAU02637	AAU02637 Synapto
16	30	100.0	202	AAU00265	AAU00265 Synapto
17	30	100.0	203	AAU02636	AAU02636 Synapto
18	30	100.0	206	AAW30103	AAW30103 Synapto
19	30	100.0	206	AAW43426	AAW43426 Mouse syn
20	30	100.0	206	AAW79198	AAW79198 Mouse syn
21	30	100.0	206	AAU00256	AAU00256 Synapto
22	30	100.0	206	AAU00261	AAU00261 Synapto
23	30	100.0	206	AAU00246	AAU00246 Synapto
24	30	100.0	206	AAU00253	AAU00253 SNARE hom
25	30	100.0	206	AAU02171	AAU02171 Synapto

26	30	100.0	206	4	AAU00266	AAU00266 Synapto
27	30	100.0	206	4	AAU02640	AAU02640 Synapto
28	30	100.0	206	4	AAU00258	AAU00258 Synapto
29	30	100.0	206	4	AAU00262	AAU00262 Synapto
30	30	100.0	206	4	AAU00259	AAU00259 Synapto
31	30	100.0	206	4	AAU00252	AAU00252 SNARE hom
32	30	100.0	206	4	AAU00260	AAU00260 Synapto
33	30	100.0	206	4	AAU02638	AAU02638 Synapto
34	30	100.0	206	4	AAU02639	AAU02639 Synapto
35	30	100.0	206	4	AAU00257	AAU00257 Synapto
36	30	100.0	206	6	AAE36662	AAE36662 Human SNA
37	30	100.0	206	6	AAE36667	AAE36667 Rat VAMP
38	30	100.0	206	7	ADE54280	ADE54280 Rat Prote
39	30	100.0	206	7	ADE54288	ADE54288 Rat Prote
40	30	100.0	206	7	ADE54276	ADE54276 Rat Prote
41	30	100.0	206	7	ADE54290	ADE54290 Human Pro
42	30	100.0	206	7	ADE54282	ADE54282 Rat Prote
43	30	100.0	206	7	ADE54274	ADE54274 Rat Prote
44	30	100.0	206	7	ADE54286	ADE54286 Human Pro
45	30	100.0	206	7	ADE54284	ADE54284 Rat Prote

ALIGNMENTS

RESULT 1

AA15582
ID AA15582 standard; peptide; 6 AA.

XX AA15582;

XX 02-MAR-2001 (first entry)

XX Human SNAP-25 N-terminal peptide #2.

XX Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.

XX Homo sapiens.

XX WO200064932-A1.

XX 02-NOV-2000.

XX 18-FEB-2000; 2000WO-ES000058.

XX 23-APR-1999; 99ES-00000844.

XX (LIPO-) LIPOTEC SA.

PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;

XX WPI; 2001-007091/01.

XX New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders.

XX Claim 9; Page 32; 40pp; Spanish.

XX The invention relates to new peptides comprising 3-30 contiguous amino
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AA15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
CC neurodegenerative disorders

SQ Sequence 6 AA;

XX PD 14-MAY-2004.
XX PF 13-NOV-2002; 2002FR-00014183.
XX PF 13-NOV-2002; 2002FR-00014183.
XX PR 13-NOV-2002; 2002FR-00014183.
XX PA (OREA) L'OREAL SA.
XX PI Renault B;
XX PT WPI; 2004-402925/38.
XX DR Topical cosmetic composition for smoothing skin wrinkles and fine lines
XX PT containing synergistic combination of peptide with sequence based on SNAP
XX PT 25 protein and calcium channel inhibitor.
XX PS Claim 4; SEQ ID NO 3; 23pp; French.
XX CC The present invention relates to novel compositions (A) for topical
XX CC application to the skin. (A) comprises physiological medium containing at
XX CC least one Synaptosomal Associated Protein 25kDa (SNAP 25) peptide (I;
XX CC ADP13166-ADP13171) and at least one calcium channel inhibitor (II). The
XX CC combination of (I) and (II) has a synergistic effect in combating
XX CC wrinkles. As well as their known anti-wrinkle activity based on SNAP
XX CC receptor complex inhibition, (I) have been found to show synergistic
XX CC effect in antagonizing type L calcium channels when used in combination
XX CC with (II) which are also known anti-wrinkle agents. (A) are used
XX CC cosmetically as topically applied agents for treating and/or preventing
XX CC (specifically smoothing) wrinkles and fine lines, especially expression
XX CC wrinkles by application to the face or forehead, particularly by
XX CC application to wrinkles and fine lines located radially around the mouth
XX CC and/or eyes, horizontally on the forehead or in the space between the
XX CC eyebrows.
XX SQ Sequence 13 AA;
Query Match 100.0%; Score 30; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
DB 3 EEMQRR 8
RESULT 5
AAG00764
ID AAG00764 standard; protein; 64 AA.
AC AAG00764;
XX 06-OCT-2000 (first entry)
XX DE Human secreted protein, SEQ ID NO: 4845.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping.
XX OS Homo sapiens.
XX OS EP1033401-A2.
XX PN 06-SEP-2000.
XX PD 21-FEB-2000; 2000EP-00200610.
XX PF 26-FEB-1999; 99US-0122487P.
XX PR (GEST) GENSET.
XX PA Dumas Milne Edwards J, Duclert A, Giordano J;
XX PI The invention relates to new peptides comprising 3-30 contiguous amino

DR WPI; 2000-500381/45.
DR N-PSDB; AAC00770.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 13; SEQ ID NO 4845; 71pp + Sequence Listing; English.
XX CC The present sequence is a polypeptide encoded by one of a large number of
XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated
XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT
XX CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX CC sequences derived from the 5' ends of mRNAs and even in those cases where
XX CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX CC are also used in diagnostic, forensic, gene therapy and chromosome
XX CC mapping procedures. They are used to obtain upstream regulatory sequences
XX CC and to design expression and secretion vectors
XX SQ Sequence 64 AA;
Query Match 100.0%; Score 30; DB 3; Length 64;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
DB 12 EEMQRR 17
RESULT 6
AAB15581
ID AAB15581 standard; peptide; 82 AA.
XX AC AAB15581;
XX XX 02-MAR-2001 (first entry)
XX DT Human SNAP-25 N-terminal peptide #1.
XX DE Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
XX KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
XX KW neurodegenerative disorder.
XX OS Homo sapiens.
XX XX WO200064932-A1.
XX PN 02-NOV-2000.
XX PD 18-FEB-2000; 2000WO-ES000058.
XX PF 23-APR-1999; 99ES-00000844.
XX PR (LIPO-) LIPOTEC SA.
XX PA Planes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
XX PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
XX PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
XX PI Perez Paya E;
XX XX WPI; 2001-007091/01.
XX DR New peptides containing amino acid sequences from known proteins for
XX PT treatment of neurological disorders.
XX PT Claim 1; Page 31; 40pp; Spanish.
XX PS The invention relates to new peptides comprising 3-30 contiguous amino

CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AAI1581-B1586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
CC neurodegenerative disorders

XX SQ Sequence 82 AA;

Query Match 100.0%; Score 30; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 11 EEMQRR 16

RESULT 7
ADP13166
ID ADP13166 standard; protein; 82 AA.

XX AC ADP13166;

DT 29-JUL-2004 (first entry)

XX DE SNAP 25 protein N-terminal domain protein, SEQ ID 1.

XX KW Dermatological; Synaptosomal Associated Protein 25kDa; SNAP 25;
XX KW anti-wrinkle.

XX OS Unidentified.

XX PN FR2846885-A1.

XX PD 14-MAY-2004.

XX PF 13-NOV-2002; 2002FR-00014183.

XX PR 13-NOV-2002; 2002FR-00014183.

XX PA (OREA) L'OREAL SA.

XX PI Renault B;

XX PS WPI; 2004-402925/38.

XX CC Topical cosmetic composition for smoothing skin wrinkles and fine lines
XX CC containing synergistic combination of peptide with sequence based on SNAP
XX CC 25 protein and calcium channel inhibitor.

XX CC Claim 4; SEQ ID NO 1; 23pp; French.

XX CC The present invention relates to novel compositions (A) for topical
XX CC application to the skin. (A) comprises physiological medium containing at
XX CC least one Synaptosomal Associated Protein 25kDa (SNAP 25) peptide (I);
XX CC ADP13166-ADP13171) and at least one calcium channel inhibitor (II). The
XX CC combination of (I) and (II) has a synergistic effect in combating
XX CC wrinkles. As well as their known anti-wrinkle activity based on SNAP
XX CC receptor complex inhibition, (I) have been found to show synergistic
XX CC effect in antagonizing type L calcium channels when used in combination
XX CC with (II) which are also known anti-wrinkle agents. (A) are used
XX CC cosmetically as topically applied agents for treating and/or preventing
XX CC (specifically smoothing) wrinkles and fine lines, especially expression
XX CC wrinkles by application to the face or forehead, particularly by
XX CC application to wrinkles and fine lines located radially around the mouth
XX CC and/or eyes, horizontally on the forehead or in the space between the
XX CC eyebrows.

XX SQ Sequence 82 AA;

Query Match 100.0%; Score 30; DB 8; Length 82;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 11 EEMQRR 16

RESULT 8
ABU43453

ID ABU43453 standard; protein; 93 AA.

XX AC ABU43453;

DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #28980.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Staphylococcus haemolyticus.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362999P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA47323.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 71377; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway;
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 30; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 24 EEMQRR 29

RESULT 9
AAG03825
ID AAG03825 standard; protein; 106 AA.

AC AAG03825;

XX 06-OCT-2000 (first entry)

DT Human secreted protein, SEQ ID NO: 7906.

DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.

XX N-PSDB; AAC03831.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7906; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX Sequence 106 AA;

Query Match 100.0%; Score 30; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

RESULT 10
AAG03826
ID AAG03826 standard; protein; 106 AA.

AC AAG03826;

XX 06-OCT-2000 (first entry)

DT Human secreted protein, SEQ ID NO: 7907.

DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.

XX N-PSDB; AAC03832.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7907; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX Sequence 106 AA;

Query Match 100.0%; Score 30; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

RESULT 11
AAU00255
ID AAU00255 standard; protein; 198 AA.

XX AAU00255;

DT 12-SEP-2001 (first entry)
 XX Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX Mus sp.
 OS Synthetic.
 XX WO200118038-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new
 CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state. Note: The present sequence is
 CC not shown in the specification but is derived from the mouse SNAP-25
 CC sequence given in figure 8 (see AAU00246)
 XX Sequence 199 AA;
 SQ Query Match 100.0%; Score 30; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 12 EEMQRR 17
 RESULT 12
 AAU00263
 ID AAU00263 standard; protein; 199 AA.

AAU00263;
 12-SEP-2001 (first entry)
 Synaptosomal-associated protein, SNAP25, mutant 1-199 (R198T).
 SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 synaptosomal-associated protein; mouse; mutant; mutein;
 N-ethylmaleimide-sensitive fusion protein;
 soluble NSF-attachment protein receptor.
 Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT WO200118038-A2.
 XX 15-MAR-2001.
 PD 18-AUG-2000; 2000WO-GB003196.
 PF 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-199 (R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX Sequence 199 AA;
 SQ Query Match 100.0%; Score 30; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6

RESULT 15
AAU02637
ID AAU02637 standard; protein; 201 AA.
XX AC AAU02637;
XX DT 12-SEP-2001 (first entry)
XX DE Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).
XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX OS Mus SP.
OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
XX WO200118038-A2.
XX PD 15-MAR-2001.
XX PF 18-AUG-2000; 2000WO-GB003196.
XX PR 20-AUG-1999; 99US-0149993P.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
XX WPI; 2001-226739/23.
XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.
XX
PS Example 1; Page; 131pp; English.
XX
CC The sequence represents the amino acid sequence of synaptosomal-
CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
CC treating a patient suffering from poisoning or at risk of poisoning by a
CC clostridial toxin, comprising supplying a SNARE (soluble (N-
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
CC a cell of the patient, where the SNARE is resistant to proteolysis by the
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
CC capable of performing SNARE-dependent exocytosis, comprises supplying a
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
CC or a recombinant polynucleotide encoding the SNARE is useful in the
CC manufacture of a medicament for the treatment of a patient suffering from
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
CC botulism or tetanus. The fragment, variant, fusion or derivative of a
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
CC either of these SNARE polypeptides are useful in the manufacture of
CC medicament for the treatment of a patient in need of inhibition of SNARE-
CC dependent exocytosis from a cell capable of performing SNARE-dependent
CC exocytosis. The method of treatment is relatively fast, thus alleviating
CC the symptoms when most severe and taking the patient out of critical
CC state. Note: The present sequence is not shown in the specification but
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
CC AAU00246)
XX
SQ Sequence 201 AA;

Query Match 100.0%; Score 30; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 12 EEMQRR 17

Search completed: February 5, 2005, 23:12:03
Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 23:09:26 ; Search time 43 Seconds
(without alignments)
10.416 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	64	4	US-09-513-999C-4845
2	30	100.0	68	4	US-09-621-976-7614
3	30	100.0	106	4	US-09-513-999C-7906
4	30	100.0	106	4	US-09-513-999C-7907
5	30	100.0	159	4	US-09-902-540-13556
6	30	100.0	206	1	US-08-393-985-18
7	30	100.0	206	3	US-08-819-286-1
8	30	100.0	206	4	US-09-949-016-6311
9	30	100.0	219	4	US-09-949-016-10671
10	27	90.0	200	4	US-09-252-991A-23347
11	27	90.0	211	4	US-09-248-796A-19812
12	27	90.0	231	4	US-09-252-991A-27366
13	27	90.0	231	4	US-09-502-540-13879
14	27	90.0	314	4	US-09-543-681A-5695
15	27	90.0	375	1	US-07-803-622E-7
16	27	90.0	375	1	US-07-803-622E-9
17	27	90.0	376	4	US-09-270-767-42071
18	27	90.0	534	4	US-09-107-532A-6549
19	27	90.0	612	3	US-09-318-794A-5
20	27	90.0	739	1	US-07-803-622E-2
21	27	90.0	868	1	US-07-864-004B-6
22	27	90.0	868	1	US-08-251-937A-6
23	27	90.0	868	1	US-08-212-133A-3
24	27	90.0	914	3	US-09-437-054A-8
25	27	90.0	961	4	US-09-538-092-1231
26	27	90.0	1031	4	US-09-902-540-16773
27	27	90.0	1065	4	US-09-949-016-11618

28	27	90.0	1090	5	PCT-US93-03275-6	Sequence 6, Appli
29	27	90.0	2115	3	US-09-324-867-5	Sequence 5, Appli
30	27	90.0	2133	2	US-08-670-707A-37	Sequence 37, Appli
31	27	90.0	2133	3	US-09-037-601-37	Sequence 37, Appli
32	27	90.0	2133	3	US-09-315-179-37	Sequence 37, Appli
33	27	90.0	2133	4	US-09-523-656-30	Sequence 30, Appli
34	26	86.7	95	4	US-09-270-767-32716	Sequence 32716, A
35	26	86.7	120	4	US-09-809-920-6	Sequence 6, Appli
36	26	86.7	253	4	US-09-252-991A-31497	Sequence 31497, A
37	26	86.7	345	4	US-09-248-796A-20780	Sequence 20780, A
38	26	86.7	362	4	US-09-107-532A-7093	Sequence 7093, Ap
39	26	86.7	363	4	US-09-252-991A-32850	Sequence 32850, A
40	26	86.7	496	4	US-09-252-991A-20207	Sequence 20207, A
41	26	86.7	496	4	US-09-540-236-3821	Sequence 3821, Ap
42	26	86.7	631	4	US-09-949-016-11595	Sequence 11595, A
43	26	86.7	728	3	US-08-915-337-2	Sequence 2, Appli
44	26	86.7	745	4	US-09-549-016-9976	Sequence 9976, Ap
45	26	86.7	746	4	US-09-248-796A-20280	Sequence 20280, A

ALIGNMENTS

RESULT 1
US-09-513-999C-4845
; Sequence 4845, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4845
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4845

Query Match 100.0%; Score 30; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 12 EEMQRR 17

RESULT 2
US-09-621-976-7614
; Sequence 7614, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7614
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-621-976-7614

Query Match 100.0%; Score 30; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 12 EEMQRR 17

RESULT 3

US-09-513-999C-7906
; Sequence 7906, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7906
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 71
; OTHER INFORMATION: Xaa=Met or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa=Gly or Val
; US-09-513-999C-7906

Query Match 100.0%; Score 30; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 12 EEMQRR 17

RESULT 4

US-09-513-999C-7907
; Sequence 7907, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7907

LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 71
; OTHER INFORMATION: Xaa=Met or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa=Gly or Val
; US-09-513-999C-7907

Query Match 100.0%; Score 30; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 12 EEMQRR 17

RESULT 5

US-09-902-540-13556
; Sequence 13556, Application US/09902540
; Patent No. 683447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wisegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13556
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-13556

Query Match 100.0%; Score 30; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 147 EEMQRR 152

RESULT 6

US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 8600-0152

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-393-985-18

Query Match 100.0%; Score 30; DB 1; Length 206;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

Db 12 EEMQRR 17

RESULT 7

US-08-819-286-1

Sequence 1, Application US/08819286

Patent No. 6169074

GENERAL INFORMATION:

APPLICANT: Montal, Mauricio

TITLE OF INVENTION: PEPTIDE INHIBITORS OF

TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/819,286

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,599

FILING DATE: 18-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Taylor, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07349/005001

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-819-286-1

Query Match 100.0%; Score 30; DB 3; Length 206;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

Db 12 EEMQRR 17

RESULT 8

US-09-949-016-6311

Sequence 6311, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6311

LENGTH: 206

TYPE: PRT

ORGANISM: Human

US-09-949-016-6311

Query Match 100.0%; Score 30; DB 4; Length 206;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

Db 12 EEMQRR 17

RESULT 9

US-09-949-016-10671

Sequence 10671, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10671

LENGTH: 219

TYPE: PRT

ORGANISM: Human

US-09-949-016-10671

Query Match 100.0%; Score 30; DB 4; Length 219;

Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 25 EEMQRR 30

RESULT 10
US-09-252-991A-23347
; Sequence 23347, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23347
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23347

Query Match 90.0%; Score 27; DB 4; Length 200;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 86 EELQRR 91

RESULT 11
US-09-248-796A-19812
; Sequence 19812, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19812
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19812

Query Match 90.0%; Score 27; DB 4; Length 215;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 98 EEMQRR 103

RESULT 12
US-09-252-991A-27366
; Sequence 27366, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27366
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27366

Query Match 90.0%; Score 27; DB 4; Length 231;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 203 EELQRR 208

RESULT 13
US-09-902-540-13879
; Sequence 13879, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13879
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13879

Query Match 90.0%; Score 27; DB 4; Length 291;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 249 EELQRR 254

RESULT 14
US-09-543-681A-5695
; Sequence 5695, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

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; SEQ ID NO 5695
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5695

Query Match          90.0%; Score 27; DB 4; Length 314;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEMQRR 6
Db      135 EELQRR 140

RESULT 15
US-07-803-622E-7
; Sequence 7, Application US/07803622E
; Patent No. 5525497
; GENERAL INFORMATION:
; APPLICANT: Keller, Walter
; APPLICANT: Lingner, Joachim
; APPLICANT: Martin, Georges
; APPLICANT: Wahle, Elmar
; TITLE OF INVENTION: RECOMBINANT POLY(A) POLYMERASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803,622E
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 195/296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-803-622E-7

Query Match          90.0%; Score 27; DB 1; Length 375;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EEMQRR 6
Db      56 EELQRR 61

Search completed: February 5, 2005, 23:24:47
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 23:12:52 ; Search time 129 Seconds
(without alignments)
15.149 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 REMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	100.0	206	10	US-09-942-024-2
3	30	100.0	206	10	US-09-942-024-7
4	30	100.0	206	10	US-09-942-024-12
5	30	100.0	206	10	US-09-942-024-2
6	30	100.0	206	10	US-09-942-024-7
7	30	100.0	206	10	US-09-942-024-12
8	30	100.0	206	15	US-10-261-161-4
9	30	100.0	206	15	US-10-261-161-5
10	30	100.0	206	15	US-10-261-161-109
11	30	100.0	206	16	US-10-318-417-3
12	30	100.0	249	10	US-09-942-024-16
13	30	100.0	249	10	US-09-942-024-16

14	30	100.0	249	15	US-10-261-161-9
15	27	90.0	35	13	US-10-029-217A-21
16	27	90.0	82	14	US-10-082-828A-255
17	27	90.0	101	15	US-10-424-599-162440
18	27	90.0	101	16	US-10-437-963-179345
19	27	90.0	149	15	US-10-424-599-208350
20	27	90.0	180	15	US-10-424-599-186497
21	27	90.0	185	16	US-10-437-963-144759
22	27	90.0	205	15	US-10-424-599-237624
23	27	90.0	210	16	US-10-437-963-141286
24	27	90.0	213	16	US-10-767-701-43626
25	27	90.0	214	9	US-09-925-300-1287
26	27	90.0	215	16	US-10-437-963-106246
27	27	90.0	222	16	US-10-437-963-131892
28	27	90.0	240	14	US-10-029-386-33812
29	27	90.0	245	9	US-09-925-299-791
30	27	90.0	245	10	US-09-925-299-791
31	27	90.0	252	15	US-10-282-122A-74647
32	27	90.0	257	15	US-10-282-122A-66793
33	27	90.0	282	15	US-10-425-114-60379
34	27	90.0	284	15	US-10-425-114-40902
35	27	90.0	285	15	US-10-424-599-246623
36	27	90.0	288	16	US-10-437-963-141287
37	27	90.0	300	16	US-10-437-963-165851
38	27	90.0	303	15	US-10-282-122A-67873
39	27	90.0	303	15	US-10-282-122A-69610
40	27	90.0	308	16	US-10-437-963-192256
41	27	90.0	323	16	US-10-437-963-103645
42	27	90.0	345	14	US-10-156-761-10629
43	27	90.0	375	16	US-10-437-963-154851
44	27	90.0	389	14	US-10-106-698-4653
45	27	90.0	391	15	US-10-424-599-237591

ALIGNMENTS

RESULT 1

US-10-282-122A-71377
Sequence 71377, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Cart, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931

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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71377
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71377

Query Match      100.0%; Score 30; DB 15; Length 93;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
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Db      24 EEMQRR 29

RESULT 2
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      12 EEMQRR 17

RESULT 3
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7
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Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      12 EEMQRR 17

RESULT 4
US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-12

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      12 EEMQRR 17

RESULT 5
US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
        |||||
Db      12 EEMQRR 17

RESULT 6
US-09-942-098-7
; Sequence 7, Application US/09942098
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; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-098-7

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

RESULT 7
US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match      100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

RESULT 8
US-10-261-161-4
; Sequence 4, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-261-161-4

Query Match      100.0%; Score 30; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

RESULT 9
US-10-261-161-5
; Sequence 5, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-261-161-5

Query Match      100.0%; Score 30; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

RESULT 10
US-10-261-161-109
; Sequence 109, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-261-161-109

Query Match      100.0%; Score 30; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17
```

```
RESULT 11
US-10-318-417-3
; Sequence 3, Application US/10318417
; Publication No. US20040115727A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Evolved Clostridial Toxins With Altered
; TITLE OF INVENTION: Protease Specificity
; FILE REFERENCE: P-AR 4670
; CURRENT APPLICATION NUMBER: US/10/318,417
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-417-3
Query Match 100.0%; Score 30; DB 16; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 12
US-09-942-024-16
; Sequence 16, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-024-16
Query Match 100.0%; Score 30; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 13
US-09-942-098-16
; Sequence 16, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-098-16
Query Match 100.0%; Score 30; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 14
US-10-261-161-9
; Sequence 9, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-261-161-9
Query Match 100.0%; Score 30; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 15
US-10-029-217A-21
; Sequence 21, Application US/10029217A
; Publication No. US20020164735A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC N.
; APPLICANT: WANG, DA-ZHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
; TITLE OF INVENTION: NUCLEAR REGULATORY FACTOR
; FILE REFERENCE: UTSD:695US
; CURRENT APPLICATION NUMBER: US/10/029,217A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/257,761
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-217A-21
Query Match 90.0%; Score 27; DB 13; Length 35;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 EEMQRR 6
| | | |
Db 11 EELQRR 16

Search completed: February 5, 2005, 23:27:28
Job time : 130 secs

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OM protein - protein search, using sw model

Run on: February 5, 2005, 22:37:00 ; Search time 38 seconds
(without alignments)
15.192 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	56	2 S36812	probable synapse-a
2	30	100.0	149	2 D95399	protein [imported]
3	30	100.0	206	2 A37861	synaptosomal-aasoc
4	30	100.0	206	2 I53735	nerve terminal pro
5	30	100.0	206	2 I67823	nerve terminal pro
6	30	100.0	206	2 A33623	synaptosomal-aasoc
7	30	100.0	249	2 S38308	SNAP-25 protein -
8	30	100.0	249	2 S38309	SNAP-25 protein -
9	27	90.0	112	2 T34589	hypothetical prote
10	27	90.0	117	2 C87594	hypothetical prote
11	27	90.0	162	1 F70358	hydrogenase matura
12	27	90.0	257	2 C83005	conserved hypothet
13	27	90.0	264	2 D75298	carbonic anhydrase
14	27	90.0	283	2 S42393	G-box-binding prot
15	27	90.0	303	2 S58243	pyrroloquinoline q
16	27	90.0	309	2 E69200	conserved hypothet
17	27	90.0	319	2 C83892	proline dehydrogen
18	27	90.0	337	2 T06602	hypothetical prote
19	27	90.0	333	2 T05121	hypothetical prote
20	27	90.0	378	2 JC5658	LIM domain-contain
21	27	90.0	407	2 C97212	HD GYP hydrolase d
22	27	90.0	450	2 C75033	adenylosuccinate l
23	27	90.0	450	2 H71135	probable adenylosu
24	27	90.0	453	2 S52690	hypothetical prote
25	27	90.0	472	2 AB3239	conserved hypothet
26	27	90.0	509	2 A71254	probable glu-tRNA
27	27	90.0	528	2 B75310	conserved hypothet
28	27	90.0	534	2 T39903	serine-rich protei
29	27	90.0	622	2 S51972	SPC72 protein - ye

30 27 90.0 647 2 C71534 probable transglyc
31 27 90.0 689 2 S17875 polynucleotide ade
32 27 90.0 702 2 C69999 DNA translocase et
33 27 90.0 727 2 S54512 hypothetical prote
34 27 90.0 739 2 S18642 polynucleotide ade
35 27 90.0 740 2 S17925 polynucleotide ade
36 27 90.0 783 2 AF1275 DNA translocase ho
37 27 90.0 784 2 AF1638 DNA translocase ho
38 27 90.0 809 1 Q0BE34 BBLF4 protein - hu
39 27 90.0 856 2 T13159 E1B-sskba-associat
40 27 90.0 869 2 A25945 coagulation factor
41 27 90.0 947 2 B86231 hypothetical prote
42 27 90.0 961 2 A55380 facio-genital dyspl
43 27 90.0 1203 2 T21275 hypothetical prote
44 27 90.0 1274 2 A89959 hypothetical prote
45 27 90.0 1328 2 AE2351 protoporphyrin IX

ALIGNMENTS

RESULT 1

S36812

probable synapse-associated 28K protein - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999

C;Accession: S36812

R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T

FEBS Lett. 330, 236-240, 1993

A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presy

A;Reference number: S36811; MUID:93374072; PMID:8365494

A;Accession: S36812

A;Molecule type: protein

A;Residues: 1-56 <HOR>

A;Experimental source: brain

Query Match 100.0%; Score 30; DB 2; Length 56;

Best Local Similarity 100.0%; Pred. No. 8.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

DB 2 EEMQRR 7

RESULT 2

D95399

protein [imported] - Sinorhizobium meliloti (strain 1021) magaplaamid pSymA

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: D95399

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9886, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: D95399

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-149 <KUR>

A;Cross-references: UNIPROT:Q92XY8; GB:AE006469; PIDN:AAK65758.1; PID:g14524256; GSPDB:

A;Experimental source: strain 1021, megaplaamid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler

peira, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Sma2009

A;Genome: plasmid

Query Match 100.0%; Score 30; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||

Db 137 EEMQRR 142

RESULT 3

A37861
synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37861
R;Catsicag, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of a conserved cell-type-specific protein in nerve terminals coincides
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||

Db 12 EEMQRR 17

RESULT 4

I53735
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I53735
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; GB:L19760; NID:g307425; PIDN:AAC37545.1; PID:g307426
C;Genetics:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||

Db 12 EEMQRR 17

RESULT 5

I67823
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994

A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; GB:L19761; NID:g307427; PIDN:AAC37546.1; PID:g307428
C;Genetics:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||

Db 12 EEMQRR 17

RESULT 6

A33623
synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differs
A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1;

Query Match 100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||

Db 12 EEMQRR 17

RESULT 7

S38308
SNAP-25 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S38308
R;Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding di
A;Reference number: S38308; MUID:93389738; PMID:8377193
A;Accession: S38308
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <BAR>
A;Cross-references: EMBL:I09250
C;Genetics:
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 30; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||

Db 12 EEMQRR 17

RESULT 8

S38309
SNAP-25 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S38309
R;Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding disulfide isomerase
A;Reference number: S38308; MUID:93389738; PMID:8377193
A;Accession: S38309
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <BAR>
A;Cross-references: EMBL:L09250
C;Genetics:
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 30; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 9

T34589
hypothetical protein SC10A5.22 SC10A5.22 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34589
R;Murphy, L.; Harris, D.; Parthill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21548
A;Accession: T34589
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-112 <MUR>
A;Cross-references: UNIPROT:O54113; EMBL:AL021529; PIDN:CAA16454.1; GSPDB:GN000070; SCOPB:1A01
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC10A5.22

Query Match 90.0%; Score 27; DB 2; Length 112;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 97 EELQRR 102

RESULT 10

C87594
hypothetical protein CC2787 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87594
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87594
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <STO>
A;Cross-references: UNIPROT:Q9MAP3; GB:AE005673; MID:gl3424387; PIDN:AAK24751.1; GSPDB:G
C;Genetics:
A;Gene: CC2787

Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 74 DEMQRR 79

RESULT 11

F70358
hydrogenase maturation factor hupD [similarity] - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2003
C;Accession: F70358
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; S.
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70358
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-162 <AQF>
A;Cross-references: GB:AE000701; GB:AE000657; MID:g2983260; PIDN:AAC06858.1; PID:g29832
A;Experimental source: strain VF5
C;Genetics:
A;Gene: hupD
C;Superfamily: [NiFe]-hydrogenase maturation protease

Query Match 90.0%; Score 27; DB 1; Length 162;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 23 EELQRR 28

RESULT 12

C83005
conserved hypothetical protein PA5135 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83005
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83005
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Cross-references: UNIPROT:Q9HU49; GB:AE004926; GB:AE004091; MID:g9951424; PIDN:AAAG085
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA5135

Query Match 90.0%; Score 27; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 143 EELQRR 148

RESULT 13

D75298
carbonic anhydrase - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75298
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <WHI>
A;Cross-references: UNIPROT:Q9RS89; GB:AE002056; GB:AE000513; NID:g6460037; PIDN:AAF1178
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2238
A;Map position: 1
C;Superfamily: Escherichia coli carbonate dehydratase

Query Match 90.0%; Score 27; DB 2; Length 264;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
||:||||
Db 34 EELQRR 39

RESULT 14

S42393
G-box-binding protein - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42393
R;Meier, I.; Gruissem, W.
Nucleic Acids Res. 22, 470-478, 1994
A;Title: Novel conserved sequence motifs in plant G-box binding proteins and implication
A;Reference number: S42392; MUID:94173701; PMID:8127687
A;Accession: S42393
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-283 <MEI>
A;Cross-references: UNIPROT:Q43508; EMBL:X74942; NID:g456752; PIDN:CAA52896.1; PID:g4567
C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
F;182-222/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 90.0%; Score 27; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
||:||||
Db 213 EELQRR 218

RESULT 15

S58243
pyrroloquinoline quinone synthesis B - Pseudomonas fluorescens
C;Species: Pseudomonas fluorescens
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58243
R;Schneider, U.; Keel, C.; Defago, G.; Haas, D.
submitted to the EMBL Data Library, May 1995
A;Description: Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0: thei
A;Reference number: S58239
A;Cross-references: UNIPROT:P55172; EMBL:X87299; NID:g929799; PIDN:CAA60733.1; PID:g9298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <SCH>
A;Cross-references: UNIPROT:P55172; EMBL:X87299; NID:g929799; PIDN:CAA60733.1; PID:g9298

Query Match 90.0%; Score 27; DB 2; Length 303;

Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
||:||||
Db 227 DEMQRR 232

Search completed: February 5, 2005, 23:12:47
Job time : 39 secs

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OM protein - protein search, using sw model

Run on: February 5, 2005, 23:02:51 ; Search time 170 Seconds
(without alignments)

18.073 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	18	2 Q9TRF1	Q9trf1 bos taurus
2	30	100.0	82	2 Q8IQC6	Q8iqc6 drosophila
3	30	100.0	82	2 Q8MZ33	Q8mz33 drosophila
4	30	100.0	107	2 Q8N3E7	Q8n3e7 homo sapien
5	30	100.0	149	2 Q92XY8	Q92xy8 rhizobium m
6	30	100.0	166	2 Q6QNZ0	Q6qnz0 poephila gu
7	30	100.0	206	1 SN25 CHICK	P60878 gallus gall
8	30	100.0	206	1 SN25 HUMAN	P60880 homo sapien
9	30	100.0	206	1 SN25 MACMU	P60877 macaca mula
10	30	100.0	206	1 SN25 MOUSE	P60879 mus musculus
11	30	100.0	206	1 SN25 RAT	P60881 rattus norv
12	30	100.0	206	2 Q8AXM1	Q8axm1 xenopus lae
13	30	100.0	206	2 Q8AXM2	Q8axm2 xenopus lae
14	30	100.0	206	2 Q640W4	Q640w4 xenopus lae
15	30	100.0	216	2 Q7Z390	Q7z390 homo sapien
16	30	100.0	284	2 Q67XD8	Q67kd8 symbiacte
17	30	100.0	297	2 Q8N417	Q8n417 homo sapien
18	30	100.0	344	2 Q6BYE0	Q6bye0 debaryomyce
19	30	100.0	507	2 Q8BVG8	Q8bvg8 homo sapien
20	30	100.0	537	2 Q9W2P0	Q9w2p0 drosophila
21	30	100.0	571	2 Q6MD10	Q6md10 homo sapien
22	30	100.0	576	2 Q6AS79	Q6as79 desulfotale
23	30	100.0	616	2 Q6AWA5	Q6awas homo sapien
24	30	100.0	685	2 Q6MZ15	Q6mz15 homo sapien
25	30	100.0	739	2 Q7XR86	Q7xr86 oryza sativ
26	30	100.0	753	2 Q6BGL9	Q6bgl9 paramecium
27	30	100.0	904	2 Q8IWC1	Q8iwc1 homo sapien
28	30	100.0	1142	2 Q757D1	Q757d1 ashbya goss
29	27	90.0	21	2 Q875B3	Q875b3 chimpanzee
30	27	90.0	81	2 Q7V6N4	Q7v6n4 prochloroco
31	27	90.0	87	2 Q69YU4	Q69yu4 homo sapien

32 27 90.0 87 2 Q8BT51 Q8bt51 mus musculus
33 27 90.0 88 2 Q6WHU0 Q6whu0 bacterioph
34 27 90.0 96 2 Q9NYJ1 Q9nyj1 homo sapien
35 27 90.0 101 2 Q6YSA0 Q6ysa0 oryza sativ
36 27 90.0 112 2 Q54113 Q54113 streptomyce
37 27 90.0 117 2 Q9A4P3 Q9a4p3 caulobacter
38 27 90.0 122 2 Q9BTB7 Q9btb7 homo sapien
39 27 90.0 127 2 Q7MQZ1 Q7mqz1 wolinnella s
40 27 90.0 128 2 Q8PFC6 Q8pfc6 xanthomonas
41 27 90.0 130 2 Q76943 Q76943 human immun
42 27 90.0 135 2 Q8P3U7 Q8p3u7 xanthomonas
43 27 90.0 148 2 Q84MC4 Q84mc4 arabidopsis
44 27 90.0 154 2 Q72DP7 Q72dp7 desulfovibr
45 27 90.0 162 2 Q66898 Q66898 aquifex aeo

ALIGNMENTS

RESULT 1

Q9TRF1 PRELIMINARY; PRT; 18 AA.
AC Q9TRF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Soluble N-ethylmaleimide-sensitive attachment protein SNAP-25
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93374072; PubMed=8365494; DOI=10.1016/0014-5793(93)80281-X;
RA Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tsugita A., Odani S.,
RA Abe T.;
RL FEBS Lett. 330:236-240(1993).
SQ SEQUENCE 18 AA; 2120 MW; 371FC93766C4A7BB CRC64;

Query Match 100.0%; Score 30; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6

Db 2 EEMQRR 7

RESULT 2

Q8IQC6 PRELIMINARY; PRT; 82 AA.
AC Q8IQC6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG32039-PA.
ORFNames=CG32039;
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Smith T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA Patel S., Sides R., Lavery T., Muzny D.M., Nelson C.R.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirska R., Tabor P.E., Wan K., Scapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirska R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Scapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003552; AN11959.1; --
 DR FlyBase; FBgn0052039; CG32039.
 SQ SEQUENCE 82 AA; 9540 MW; E0FE73104AC0796E CRC64;
 Query Match 100.0%; Score 30; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 58 EEMQRR 63
 RESULT 3
 Q8MZ33 PRELIMINARY; PRT; 82 AA.
 ID Q8MZ33
 AC Q8MZ33;
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
 DE RE03722p.
 GN ORFNames=CG32039;
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY113381; BAM39386.1; --
 DR FlyBase; FBgn0052039; CG32039.
 SQ SEQUENCE 82 AA; 9539 MW; E0F4D3104060796E CRC64;
 Query Match 100.0%; Score 30; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 58 EEMQRR 63
 RESULT 4
 Q8N3E7 PRELIMINARY; PRT; 107 AA.
 ID Q8N3E7
 AC Q8N3E7;
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DE Hypothetical protein DKFZp76111323 (Fragment).
 GN Name=DKFZp76111323;
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Amalgam;
 RG The German cDNA Consortium;
 RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL834393; CAD39055.1; --
 KW Hypothetical protein.

```

FT NON TER 1 1
SQ SEQUENCE 107 AA; 13460 MW; A411B3F036789795 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 94 EEMQRR 99

RESULT 5
ID Q92XY8 PRELIMINARY; PRT; 149 AA.
AC Q92XY8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN ORFNames=SMa2009;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowler L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR EMBL; AE007296; AAK65758.1; -.
DR PIR; D95399;
DR InterPro; IPR004360; Gly_bleo_diox.
DR Pfam; PF00903; Glyoxalase; 1.
SQ SEQUENCE 149 AA; 16237 MW; 86C045BFD8F5ACF5 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 137 EEMQRR 142

RESULT 6
ID Q6QN20 PRELIMINARY; PRT; 166 AA.
AC Q6QN20;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SNAP-25b (Fragment).
OS Neophila guttata (Zebra finch) (Taeniopygia guttata).
OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Estrildinae; Taeniopygia.
OX NCBI_TaxID=59729;
RN [1]
RP SEQUENCE FROM N.A.
RA Voigt C., Metzdorf R., Gahr M.;
RT "Differential expression pattern and steroid hormone sensitivity of
RT SNAP-25 and synaptoporin mRNA in the telencephalic song control
RT nucleus HVC of the zebra finch.";
J. Comp. Neurol. 0:0-0(2004).
-1- SIMILARITY: Belongs to the SNAP-25 family.
EMBL; AY531112; AAS21684.1; -.
GO; GO:0019717; C-synaptoosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 1.
DR PROSITE; PS50192; T-SNARE; 2.
KW Synaptoosome.
FT NON_TER 1 1
FT NON_TER 166 166
SQ SEQUENCE 166 AA; 18793 MW; 04F06E677D7BC1C7 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 5 EEMQRR 10

RESULT 7
SN25 CHICK STANDARD; PRT; 206 AA.
ID SN25 CHICK STANDARD; PRT; 206 AA.
AC P60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Synaptoosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN Names=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SNAP25B).
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=192470;
RA Catsicas S., Larhammer D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.;
RT "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP25A AND SNAP25B).
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein.";
RL J. Mol. Biol. 233:67-76(1993).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXB6 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60878-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60878-2, P13795-2;

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CC      Sequence-VSP 010018;
CC      -I- PTM: Palmitoylated (By similarity).
CC      -I- SIMILARITY: Belongs to the SNAP-25 family.
CC      -I- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M57957; AAA49072.1; -.
DR      EMBL; L09253; AAA49070.1; -.
DR      EMBL; L09254; AAA49070.1; JOINED.
DR      EMBL; L09257; AAA49070.1; JOINED.
DR      EMBL; L09259; AAA49070.1; JOINED.
DR      EMBL; L09251; AAA49070.1; JOINED.
DR      EMBL; L09258; AAA49070.1; JOINED.
DR      EMBL; L09250; AAA49070.1; JOINED.
DR      EMBL; L09253; AAA49071.1; -.
DR      EMBL; L09254; AAA49071.1; JOINED.
DR      EMBL; L09257; AAA49071.1; JOINED.
DR      EMBL; L09259; AAA49071.1; JOINED.
DR      EMBL; L09252; AAA49071.1; JOINED.
DR      EMBL; L09256; AAA49071.1; JOINED.
DR      EMBL; L09258; AAA49071.1; JOINED.
DR      PIR; A37861; A37861.
DR      GO; GO:0007269; P:neurotransmitter secretion; NAS.
DR      GO; GO:0001504; P:neurotransmitter uptake; NAS.
DR      GO; GO:0007268; P:synaptic transmission; NAS.
DR      GO; GO:0016081; P:synaptic vesicle docking; NAS.
DR      InterPro; IPR000928; SNAP-25.
DR      PROSITE; PS0192; T SNARE; 2.
DR      Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Repeat;
KW      Synaptosome.
FT      DOMAIN 19 81 t-SNARE coiled-coil homology 1;
FT      DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT      SITE 85 92 Cys-rich.
FT      SITE 180 181 Cleavage (by BONT/E) (By similarity).
FT      VARSPLIC 58 89 ERIEGRMDQINKDMKEAKNLTDLGKFGCLGV -> DRVVEE
FT      FT GNHINQDMKEAKNLTDLGKCGCLFI (in isoform
FT      SNAP-25a).
FT      /FTID:VSP_010018.
SQ      SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 EEMQRR 6
Db      12 EEMQRR 17
RESULT 8
SN25 HUMAN STANDARD; PRT; 206 AA.
ID      P0880; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DE      Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN      Names-SNAP25; Synonyms-SNAP;
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RC      TISSUE=Brain;

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RX      MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
RA      Bark I.C., Wilson M.C.;
RT      "Human cDNA clones encoding two different isoforms of the nerve
RL      terminal protein SNAP-25.";
RL      Gene 139:291-292 (1994).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
RC      TISSUE=Brain;
RX      MEDLINE=94333329; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2;
RA      Zhao N., Hashida H., Takahashi N., Sakaki Y.;
RT      "Cloning and sequence analysis of the human SNAP25 cDNA.";
RL      Gene 145:313-314 (1994).
RN      [3]
RP      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC      TISSUE=Skeletal muscle;
RX      MEDLINE=96332494; PubMed=8760387;
RA      Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA      Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA      Ward C.W.;
RT      "Insulin-responsive tissues contain the core complex protein SNAP-25
RT      (synaptosomal-associated protein 25) A and B isoforms in addition to
RL      syntaxin 4 and synaptobrevins 1 and 2.";
RL      Biochem. J. 317:945-954 (1996).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA      Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA      Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA      Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA      Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA      Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA      Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA      Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA      Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA      Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA      Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA      Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA      Huxley E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA      Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA      Leivaesalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA      Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA      Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA      Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA      Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA      Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA      Skuce C.D., Smith M.D., Soderlund C., Steward C.A., Sulston J.E.,
RA      Swann R.D., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA      Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA      Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA      Wilting L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA      Rogers J.;
RT      "The DNA sequence and comparative analysis of human chromosome 20.";
RL      Nature 414:865-871 (2001).
RN      [5]
RP      SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC      TISSUE=Eye;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udgin T.B., Toshyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighan S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kettner M., Maman A., Rodriguez S., Sanchez A.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX
RX WITH STX1A; CPLX1 AND VAMP2, AND NMR ANALYSIS.
RY MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273(02)00583-4;
RA Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RA Suedhof T.C., Rizo J.;
RT "Three-dimensional structure of the complexin/SNARE complex.";
RL Neuron 33:397-409(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXBP6.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Names=SNAP-25b;
CC IsoId=P60880-1, P13795-1;
CC Sequences=Displayed;
CC Names=SNAP-25a;
CC IsoId=P60880-2, P13795-2;
CC Sequences=VSP_006186;
CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus,
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -1- PTM: Palmitoylated (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L19760; AAC37545.1; -;
CC EMBL; L19761; AAC37546.1; -;
CC EMBL; D21267; BAA22370.1; -;
CC EMBL; AL023913; CAC34534.1; -;
CC EMBL; AL023913; CAC34535.1; -;
CC EMBL; AL023913; CAD56158.1; -;
CC EMBL; AL023913; CAB42860.1; -;
CC EMBL; BC010647; AAH10847.1; -;
CC FIR; I53735; I53735.
CC PIR; I67823; I67823.
CC PDB; 1KIL; X-ray; -;
CC Genew; HGNC:11132; SNAP25.
CC H-InvDB; HIX0015639; -;
CC MIM; 600322; -;
CC GO; GO:0007269; P:neurotransmitter secretion; NAS.
CC GO; GO:0001504; P:neurotransmitter uptake; NAS.
CC GO; GO:0007268; P:synaptic transmission; NAS.
CC GO; GO:0016081; P:synaptic vesicle docking; NAS.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC PROSITE; PS50192; T-SNARE; 2.
CC 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
KW Palmitate; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT SITE 85 92 Cys-rich.
FT SITE 180 181 Cleavage (by BONT/E).
FT VARSPLIC 58 89 ERIEAGMDQINKMKEAKNLKDLGKCGCLCV -> DRVVEE

FT FT
FT FT
FT FT
FT FT
SQ
Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
Db 12 EEMQRR 17
RESULT 9
SN25_MACMU STANDARD; PRT; 206 AA.
ID SN25 MACMU P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXBP6 (By similarity).
CC -1- PTM: Palmitoylated (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF240770; AAF64477.1; -;
CC GO; GO:0007269; P:neurotransmitter secretion; NAS.
CC GO; GO:0001504; P:neurotransmitter uptake; NAS.
CC GO; GO:0007268; P:synaptic transmission; NAS.
CC GO; GO:0016081; P:synaptic vesicle docking; NAS.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC PROSITE; PS50192; T-SNARE; 2.
CC Coiled coil; Lipoprotein; Palmitate; Repeat; Synaptosome.
KW DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT DOMAIN 85 92 Cys-rich.
FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
DB 12 EEMQRR 17

RESULT 10
SN25 MOUSE
ID SN25 MOUSE STANDARD; PRT: 206 AA.
AC P60879; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN Name=Snap25; Synonyms=Snap;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC STRAIN=BALB/c;
RX MEDLINE=90078337; PubMed=252413; DOI=10.1083/jcb.109.6.3039;
RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
RA Bloom F.E., Wilson M.C.;
RT "The identification of a novel synaptosomal-associated protein, SNAP-
RT 25, differentially expressed by neuronal subpopulations.";
RL J. Cell Biol. 109:3039-3052(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC STRAIN=ILS, and ISS;
RX MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-throughput sequence identification of gene coding variants
RT within alcohol-related QTLs.";
RL Mamm. Genome 12:657-663(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
RC STRAIN=C57BL/6J; Tissue=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gliss C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC STRAIN=C57BL/6; Tissue=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH SNAP25BP.
RX PubMed=10195194; DOI=10.1038/5673;
RA Ilardi J.M., Mochida S., Sheng Z.H.;
RT "Snapin: a SNARE-associated protein implicated in synaptic
RT transmission.";
RL Nat. Neurosci. 2:119-124(1999).
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM5, RIMS1
CC and SNAP25BP. Binds STXBP6 (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60879-1, P13795-1;
CC Sequence=Displaced;
CC Name=SNAP-25a;
CC IsoId=P60879-2, P13795-2;
CC Sequence=VSP 010019;
CC -!- PTM: palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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EMBL: M22012; AAA61741.1; -.
EMBL: AF483516; AAL90790.1; -.
EMBL: AF483517; AAL90791.1; -.
EMBL: AK078038; AAC37105.1; -.
EMBL: BC018249; AAI18249.1; -.
PIR: A33623; A33623.
MGD: MGI:98331; Snap25.
GO: GO:0007269; P:neurotransmitter secretion; NAS.
GO: GO:0001504; P:neurotransmitter uptake; NAS.
GO: GO:0007268; P:synaptic transmission; NAS.
GO: GO:0016081; P:synaptic vesicle docking; NAS.
InterPro: IPR000928; SNAP-25.
InterPro: IPR000727; T_SNARE.
PROSITE: PS50192; T_SNARE; 2.

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KW Alternative splicing; Coiled coil; Lipoprotein; Palmitate; Repeat;
FT Synaptosome. 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT DOMAIN 85 92 Cys-rich.
FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
FT VARSPLIC 58 89 ERIEEDQMDQINKMKAEKNLIDGKFCGLCV -> DRVBE
FT GMNHINQDMKEAEKNLIDGKFCGLFI (in isoform
FT SNAP-25a).
FT /FTid=VSP_010019.
SQ SEQUENCE 206 AA; 23315 MW; PBE2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
Db 12 EEMQRR 17
RESULT 11
SN25_RAT
ID SN25_RAT STANDARD; PRT; 206 AA.
AC P60881; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN Name=Snap25; Synonyms=Snap;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RA Kataoka M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC TISSUE=Brain;
RA Cho A.R., You K.H.;
RL "Cloning of the SNAP-25 gene from a rat brain cDNA library."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
RC TISSUE=Brain;
RX MEDLINE=99155074; PubMed=10037470;
RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
RT "SNARE complex proteins, including the cognate pair VAMP-2 and
RT syntaxin-4, are expressed in cultured oligodendrocytes."
RL J. Neurochem. 72:988-998(1999).
RN [4]
RP PALMITOYLATION.
RX MEDLINE=93100552; PubMed=1281490;
RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
RT methionine-rich polypeptide in rapid axonal transport and a major
RT substrate for palmitoylation in adult CNS."
RL J. Neurosci. 12:4634-4641(1992).
RN [5]
RP SUBCELLULAR LOCATION OF RNA TRANSCRIPTS.
RX MEDLINE=96346613; PubMed=8738135; DOI=10.1016/0169-328X(95)00272-T;
RA Jacobsson G., Pihl F., Bark I.C., Zhang X., Meister B.;
RT "Differential subcellular localization of SNAP-25a and SNAP-25b RNA
RT transcripts in spinal motoneurons and plasticity in expression after
RT nerve injury."
RL Brain Res. Mol. Brain Res. 37:49-62(1996).
RN [6]
RP INTERACTION WITH RIMS1.
RX MEDLINE=21413925; PubMed=11438518; DOI=10.1074/jbc.M100929200;
RA Coppola T., Magnin-Luethi S., Perret-Menoud V., Gattesco S.,
RA Schiavo G., Regazzi R.;

RT "Direct interaction of the Rab3 effector RIM with Ca2+ channels, SNAP-
RT 25, and synaptotagmin.";
RL J. Biol. Chem. 276:32756-32762(2001).
RN [7]
RP INTERACTION WITH STXBPF6.
RX MEDLINE=22140381; PubMed=12145319; DOI=10.1074/jbc.M204929200;
RA Scales S.J., Heiser B.A., Masuda E.S., Scheller R.H.;
RT "Amisyn, a novel syntaxin-binding protein that may regulate SNARE
RT complex assembly.";
RL J. Biol. Chem. 277:28271-28279(2002).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-83 AND 120-206 IN COMPLEX
RP WITH STX1A AND VAMP2.
RX MEDLINE=98430524; PubMed=9759724; DOI=10.1038/26412;
RA Sutton R.B., Faehauer D., Jahn R., Brunger A.T.;
RT "Crystal structure of a SNARE complex involved in synaptic exocytosis
RT at 2.4 A resolution.";
RL Nature 395:347-353(1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-83 IN COMPLEX WITH STX1A.
RX MEDLINE=21538870; PubMed=11533035; DOI=10.1074/jbc.M106853200;
RA Misura K.M.S., Gonzalez L.C. Jr., May A.P., Scheller R.H., Weiss W.I.;
RT "Crystal structure and biophysical properties of a complex between the
RT N-terminal SNARE region of SNAP25 and syntaxin 1a.";
RL J. Biol. Chem. 276:41301-41309(2001).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 7-83 AND 141-204 IN COMPLEX
RP WITH STX1A AND VAMP2.
RX MEDLINE=22499607; PubMed=12496247; DOI=10.1074/jbc.M211889200;
RA Ernst J.A., Brunger A.T.;
RT "High resolution structure, stability, and synaptotagmin binding of a
RT truncated neuronal SNARE complex.";
RL J. Biol. Chem. 278:8630-8636(2003).
CC -I- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -I- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXBPF6.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60881-1, P13795-1;
CC Sequences=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60881-2, P13795-2;
CC Sequences=VSP_010020;
CC -I- PTM: Palmitoylated.
CC -I- SIMILARITY: Belongs to the SNAP-25 family.
CC -I- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB003991; BAA20151.1; -;
CC EMBL; AB003992; BAA20152.1; -;
CC EMBL; AF245227; AAF81202.1; -;
CC EMBL; U56262; AAA99826.1; -;
CC EMBL; U56261; AAA99825.1; -;
CC PDB; 1JTH; X-ray; -;
CC PDB; 1N7S; X-ray; -;
CC PDB; 1SFC; X-ray; -;
CC PDB; 2BUO; Model; -;
CC RGD; 3728; Snap25.

DR GO; GO:0007269; P:neurotransmitter secretion; NAS.
 DR GO; GO:0001504; P:neurotransmitter uptake; NAS.
 DR GO; GO:0007268; P:synaptic vesicle docking; NAS.
 DR GO; GO:0016081; P:synaptic vesicle docking; NAS.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T SNARE.
 DR PROSITE; PS0192; T SNARE; 2.
 KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
 KW Palmitate; Repeat; Synaptosome.
 FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
 FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
 FT DOMAIN 85 92 Cys-rich.
 FT SITE 180 181 Cleavage (by BONT/E) (by similarity).
 FT VARSPIC 58 89 ERIEGMDQINKMEAKNLDLKGKGLV -> DRVVE
 FT GNHINQDMKAEKNDLKGKGLFI (in isoform
 FT GMAP-25a).
 FT /FTId=VSP_010020.
 FT HELIX 7 82
 FT HELIX 142 201
 FT TURN 202 202
 FT TURN 202 202
 SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
 Query Match 100.0%; Score 30; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 DB 12 EEMQRR 17
 RESULT 12
 Q8AXM1 PRELIMINARY; PRT; 206 AA.
 AC Q8AXM1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE SNAP25b (Snap25-prov protein)
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RT Dev. Dyn. 225:384-391 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 DR EMBL; AF335587; AA033789.1; -.
 DR EMBL; BC055981; AAHS5981.1; -.
 DR HSSP; P60881; 1JTH.
 DR GO; GO:0019717; C:synaptosome; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002197; HTH_Fis.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR010989; t-snare.
 DR InterPro; IPR000727; T SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR PRINTS; PRO1590; HTHFIS.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS0192; T_SNARE; 2.
 KW Synaptosome.
 SQ SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;
 Query Match 100.0%; Score 30; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 DB 12 EEMQRR 17
 RESULT 13
 Q8AXM2 PRELIMINARY; PRT; 206 AA.
 AC Q8AXM2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SNAP25a.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 DR EMBL; AF335586; AA013788.1; -.
 DR HSSP; P60881; 1JTH.
 DR GO; GO:0019717; C:synaptosome; IEA.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR010989; t-snare.
 DR InterPro; IPR000727; T SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS0192; T_SNARE; 2.
 KW Synaptosome.
 SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;
 Query Match 100.0%; Score 30; DB 2; Length 206;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 14

Q640W4 PRELIMINARY; PRT; 206 AA.
AC Q640W4; (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
ON NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:394-391(2002).
RN [2]

SEQUENCE FROM N.A.

RC TISSUE=Eye;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]

SEQUENCE FROM N.A.

RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082475; AAH82475.1; -;
KW Hypothetical protein.
SQ SEQUENCE 206 AA; 23115 MW; 5FF241P6DF2E9C8C CRC64;

Query Match 100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 15

Q7Z390

AC Q7Z390 PRELIMINARY; PRT; 216 AA.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686C04150 (Fragment).
GN Name=DKFZp686C04150;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human colon endothel primary cell culture;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538046; CAD97985.1; -;
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 216 AA; 24473 MW; 68CB647EB074786B CRC64;

Query Match 100.0%; Score 30; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 203 EEMQRR 208

Search completed: February 5, 2005, 23:15:43
Job time : 172 secs

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